```
1    CTGCTTCCACCAGCAAAGACCACGACTGGAGAGCCGGAGCCAGCTGGGAAACATG
     ---------+---------+---------+---------+---------+---------+   60
     GACGAAGGTGGTCGTTTCTGGTGCTGACCTCTCGGCCTCGGCCTCGTCGACCCTTTGTAC
                                                              M

61   AAGAGCGGTCTTGCTGCTGACCAGCTCCTCGTGCCTGCACACCTGGTGGCCGCCTGGAGC
     ---------+---------+---------+---------+---------+---------+   120
     TTCTCGCCAGAACGACGACTGGTCGAGGAGCACGGACGGTGTGGACCACCGGGCGGACCTCG
      K  S  V  L  L  L  T  L  Y  P  A  H  L  V  A  A  W  S

121  AATAATTATTATGCGGTGGACTGCCCTCAACACTGTGACAGCGAGTGCAAAAGCAGCCCG
     ---------+---------+---------+---------+---------+---------+   180
     TTATTAATAATACGCCACCTGACGGGAGTTGTGACACTGTCGCTCACGTTTTCGTCGGGC
      N  N  Y  A  V  D  C  P  Q  H  C  D  S  E  C  K  S  S  P

181  CGCTGCAAGAGGACAGTGCTCGACGACTGTGGCTGCCGAGTGTGCGCTGCAGGGCGG
     ---------+---------+---------+---------+---------+---------+   240
     GCGACGTTCTCCTGTCACGAGCTGCTGACACCGACGGCTCACACGCGACGTCCCGCC
      R  C  K  R  T  V  L  D  D  C  G  C  C  R  V  C  A  A  G  R
```

MATCH WITH FIG. 1B

FIG.1A

```
241
     GGAGAAACTTGCTACGGCACCAGTCTCAGGCATGGCATGGCATGAAGTGTGGCCCGGGGCTG
     ---------+---------+---------+---------+---------+---------+    300
     CCTCTTTGAACGATGGCCGTGGTCAGAGTCCGTACCTACCGTACTTCACACGGGGCCCCGAC
      G  E  T  C  Y  R  T  V  S  G  M  D  G  M  K  C  G  P  G  L

301
     AGGTGTCAGCCTTCTTAATGGGGAGGATCCTTTTGGGTGAAGAGTTTGGTATCTGCAAAGAC
     ---------+---------+---------+---------+---------+---------+    360
     TCCACAGTCGGAAGAATTACCCCTCCTAGGAAAACCACTTCTCAAACCATAGACGTTTCTG
      R  C  Q  P  S  N  G  E  D  P  F  G  E  E  F  G  I  C  K  D

361
     TGTCCCTACGGCACCTTCGGGATGGATTGCAGAGAGACCTGCAACTGCCAGTCAGGCATC
     ---------+---------+---------+---------+---------+---------+    420
     ACAGGGATGCCGTGGAAGCCCTACCTAACGTCTCTCTGGACGTTGACGGTCAGTCCGTAG
      C  P  Y  G  T  F  G  M  D  C  R  E  T  C  N  C  Q  S  G  I

421
     TGTGACAGGGGGACGGGGGAAAATGCCTGAAATTCCCTTCTTCCAATATTCAGTAACCAAG
     ---------+---------+---------+---------+---------+---------+    480
     ACACTGTCCCCCTGCCCCTTTTACGGACTTTAAGGGAAGAAGGTTATAAGTCATTGGTTC
      C  D  R  G  T  G  K  C  L  K  F  F  F  Q  Y  S  V  T  K
```

FIG.1B

MATCH WITH FIG. 1B

481 TCTTCCAACAGATTTGTTTTCTCTCACGGGAGCATGACATGGCATCTGGAGATGGCAATATT
     ------+---------+---------+---------+---------+---------+ 540
     AGAAGGTTGTCTAAACAAAGAGAGAAGTGCCTCGTACTGTACCGTAGACCTCTACCGTTATAA
     S S N R F V S L T E H D M A S G D G N I

541 GTGAGAGAAGAAGTTGTGAAAGAGAAATGCTGCCGGGTCTCCCGTAATGAGGAAATGGTTA
     ------+---------+---------+---------+---------+---------+ 600
     CACTCTCTTCTTCAACACTTTCTTCTTACGACGGCCCAGAGGGCATTACTCCTTTACCAAT
     V R E E V K E N A A G S P V M R K W L

601 AATCCACGCTGATCCCGGCTGTGATTTCTGAGAGAAGGCTCTATTTCGTGAYTGTTCAA
     ------+---------+---------+---------+---------+---------+ 660
     TTAGGTGCGACTAGGGCCGACACTAAAGACTCTTCCGAGATAAAAGCACTRACAAGTT
     N P R *

661 CACACAGCCAACATTTTAGGAACTTTCTAGATTATAGCATAAGGACATGTAATTTTTGAA
     ------+---------+---------+---------+---------+---------+ 720
     GTGTGTCGGTTGTAAAATCCTTGAAAGATCTAATATCGTATTCCTGTACATTAAAAACTT

721 GACCAAATGTGATGCATGGTGGATCCAGAAAACAAAAGTAGGATACTTACAATCCATAA
     ------+---------+---------+---------+---------+---------+ 780
     CTGGTTTACTACGTACCACTAGGTCTCTTTGTTTTTCATCCTATGAAATGTTAGGTATT
     MATCH WITH FIG. 1D

FIG. 1C

```
781  CATCCATATGACTGAACACTTGTATGTGTTGTTAAATATTCGAATGCATGTAGATTTGT
     ----------+---------+---------+---------+---------+---------+
     GTAGGTATACTGACTTGTGAACATACACACAAACAATTTATAAGCTTACGTACATCTAAACA  840

841  TAAATGTGTGTATAGTAACACTGAAGAACTAAAAATGCAATTTAGGTAATCTTACATG
     ----------+---------+---------+---------+---------+---------+
     ATTTACACACATATCATTGTGACTTCTTGATTTTTACGTTAAATCCATTAGAATGTAC  900

901  GAGACAGGTCAACCAAAGAGGAGCTAGGCAAAGCTGAAGACCGCAGTGAGTCAAATTAG
     ----------+---------+---------+---------+---------+---------+
     CTCTGTCCAGTTGGTTTCTCCCTCGATCCGTTTCGACTTCTGGCGTCACTCAGTTTAATC  960

961  TTCTTTGACTTTGATGTACATTAATGTTGGGATATGGAATGAAGACTTAAGACAGGAGA
     ----------+---------+---------+---------+---------+---------+
     AAGAAACTGAAACTACATGTAATTACAACCCTATACTTACTTCTGAATTCTCGTCCTCT  1020

1021 AGATGGGGAGGGGGTGGGAGTGGGAAATAAAATATTAGCCCTTCCTTGGTAGTAGCTT
     ----------+---------+---------+---------+---------+---------+
     TCTACCCCTCCCCACCCTCACCCTTTATTTATAAATCGGGAAGGAACCATCCATCGAA  1080
```

FIG.1D

MATCH WITH FIG. 1D

```
1081    CTCTAGAATTTAATTRIGCTTTTTTTTTTTTTTTTGGGCTTTGGGAAAAGTCAAAATAAA
        ----------+---------+---------+---------+---------+---------+    1140
        GAGATCTTAATTAAYACGAAAAAAAAAAAACCGAAACCCTTTTCAGTTTTATTT

1141    ACAACCAGAAAACCCCTGAAGGAGTAAGATGTTTGAAGCTTATGGAAATTGAGTAACA
        ----------+---------+---------+---------+---------+---------+    1200
        TGTTGGTCTTTTGGGGACTTCCTTCATTCTACAAACTTCGAATACCTTTAAACTCATTGT

1201    AACAGCTTTGANCTGAGAGCAATTYCAAAAGGCTGCTGATGTGTAGCCCCGGGTTNCCTNT
        ----------+---------+---------+---------+---------+---------+    1260
        TTGTCGAAACTNGACTCTCGTTAARGTTTTCCGACGACTACATCGGGGGCCCAANGGANA

1261    NTCTNAAGGAC
        ----------+-    1271
        NAGANTTCCTG
```

FIG.1E

```
                1                                                    50
ce10_chick    ...MGSAGAR P.ALAAALLC LARLALGSPC PAV....CQC ...PAA.APQ
cyr6_mouse    ...MSSSTFR TLAVAVTLAH LTRLAL.STC PAA....CHC ...PLE.APK
ctgf_human    .MTAASMGPV RVAFVVLLAL CSRPAVGQNC SGP....CRC ...PDEPAPR
fisp-12       .MLASVAGPI SLAL.VLLAL CTRTATGQDC SAQ....CQC ....AAEAAPH
nov_chick     .METGGQGL  PVLLLLLLL  RPCEVSGREA ACPRPCGGRC ...PAEP.PR
ibp_3human    MQRARPTLWA AALTLLVLLR GPPVARAGAS SGGLGPVVRC EPCVARALAR
ccn-4         ........MK SVLLLTTLLV PAHLVAAWSN MYAVDCPQHC DSSECKSSPR

                51                                                   100
ce10_chick    CAPGVGLVP. ....DGCGCC KVCAKQLNED C....SRTQP CDHTKGLECN
cyr6_mouse    CAPGVGLVR. ....DGCGCC KVCAKQLNED C....SKTQP CDHTKGLECN
ctgf_human    CPAGVSLVL. ....DGCGCC RVCAKQLGEL C....TERDP CDPHRGLFCD
ccn-4         ......... ......... ......... ......... .........

                401        411
ce10_chick    RLVNDIHKFR D
cyr6_mouse    SLFNDIHKFR D
ctgf_human    YYRKMYGDMA
fisp-12       YYRKMYGDMA
nov_chick     DPMSSEAKI.
ibp3_human    .........
ccn-4         .........
```

F I G. 2